



PCT10

RAW SEQUENCE LISTING

DATE: 12/11/2002

PATENT APPLICATION: US/10/009,500A

TIME: 09:28:55

Input Set : N:\CrF4\11182002\J009500.raw

Output Set: N:\CRF4\12112002\J009500A.raw

1 <110> APPLICANT: KORDOWICZ, MARIA
 2 GUESSOW, DETLET
 3 HOFMANN, UWE
 4 PACUSZKA, TADEUSZ
 5 GARDAS, ANDRZEJ
 6 <120> TITLE OF INVENTION: HYALURONIDASE FROM THE HIRUDINARIA MANILLENSIS,
 7 ISOLATION, PURIFICATION AND RECOMBINANT METHOD OF
 8 PRODUCTION
 9 <130> FILE REFERENCE: MERCK 2332
 10 <140> CURRENT APPLICATION NUMBER: US/10/009,500A
 11 <141> CURRENT FILING DATE: 2002-04-08
 12 <160> NUMBER OF SEQ ID NOS: 20
 13 <170> SOFTWARE: PatentIn Ver. 2.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 488
 17 <212> TYPE: PRT
 18 <213> ORGANISM: Hirudinaria manillensis
 19 <400> SEQUENCE: 1
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 21 1 5 10 15
 22 Ser Glu Ser Phe His Gly Val Ala Phe Asp Ala Ser Leu Phe Ser Pro
 23 20 25 30
 24 Lys Gly Leu Trp Ser Phe Val Asp Ile Thr Ser Pro Lys Leu Phe Lys
 25 35 40 45
 26 Leu Leu Glu Gly Leu Ser Pro Gly Tyr Phe Arg Val Gly Gly Thr Phe
 27 50 55 60
 28 Ala Asn Trp Leu Phe Phe Asp Leu Asp Glu Asn Asn Lys Trp Lys Asp
 29 65 70 75 80
 30 Tyr Trp Ala Phe Lys Asp Lys Thr Pro Glu Thr Ala Thr Ile Thr Arg
 31 85 90 95
 32 Arg Trp Leu Phe Arg Lys Gln Asn Asn Leu Lys Lys Glu Thr Glu Asp
 33 100 105 110
 34 Asp Leu Val Lys Leu Thr Lys Gly Ser Lys Met Arg Leu Leu Phe Asp
 35 115 120 125
 36 Leu Asn Ala Glu Val Arg Thr Gly Tyr Glu Ile Gly Lys Lys Met Thr
 37 130 135 140
 38 Ser Thr Trp Asp Ser Ser Glu Ala Glu Lys Leu Phe Lys Tyr Cys Val
 39 145 150 155 160
 40 Ser Lys Gly Tyr Gly Asp Asn Ile Asp Trp Glu Leu Gly Asn Glu Pro
 41 165 170 175
 42 Asp His Thr Ser Ala His Asn Leu Thr Glu Lys Gln Val Gly Glu Asp
 43 180 185 190
 44 Phe Lys Ala Leu His Lys Val Leu Glu Lys Tyr Pro Thr Leu Asn Lys

mp 4-5
 Does Not Comply
 Corrected Diskette Needed

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45          195          200          205
46 Gly Ser Leu Val Gly Pro Asp Val Gly Trp Met Gly Val Ser Tyr Val
47          210          215          220
48 Lys Gly Leu Ala Asp Gly Ala Gly Asp Leu Val Thr Ala Phe Thr Leu
49          225          230          235          240
50 His Gln Tyr Tyr Phe Asp Gly Asn Thr Ser Asp Val Ser Thr Tyr Leu
51          245          250          255
52 Asp Ala Thr Tyr Phe Lys Lys Leu Gln Gln Leu Phe Asp Lys Val Lys
53          260          265          270
54 Asp Val Leu Lys Asn Ser Gln His Lys Asp Lys Pro Leu Trp Leu Gly
55          275          280          285
56 Glu Thr Ser Ser Gly Tyr Asn Ser Gly Thr Lys Asp Val Ser Asp Arg
57          290          295          300
58 Tyr Val Ser Gly Phe Leu Thr Leu Asp Lys Leu Gly Leu Ser Ala Ala
59          305          310          315          320
60 Asn Asn Val Lys Val Val Ile Arg Gln Thr Ile Tyr Asn Gly Tyr Tyr
61          325          330          335
62 Gly Leu Leu Asp Lys Asn Thr Leu Glu Pro Asn Pro Asp Tyr Trp Leu
63          340          345          350
64 Met His Val His Asn Ser Leu Val Gly Asn Thr Val Phe Lys Val Asp
65          355          360          365
66 Val Ser Asp Pro Thr Asn Lys Ala Arg Val Tyr Ala Gln Cys Thr Lys
67          370          375          380
68 Thr Asn Ser Lys His Thr Gln Ser Arg Tyr Tyr Lys Gly Ser Leu Thr
69          385          390          395          400
70 Ile Phe Ala Leu Asn Val Gly Asp Glu Asp Val Thr Leu Lys Ile Asp
71          405          410          415
72 Gln Tyr Gly Gly Lys Lys Ile Tyr Ser Tyr Ile Leu Thr Pro Glu Gly
73          420          425          430
74 Gly Gln Leu Thr Ser Gln Lys Val Leu Leu Asn Gly Lys Glu Leu Lys
75          435          440          445
76 Leu Val Ser Asp Gln Leu Pro Glu Leu Asn Ala Asn Glu Ser Lys Thr
77          450          455          460
78 Ser Phe Thr Leu Ser Pro Lys Thr Phe Gly Phe Phe Val Val Ser Asp
79          465          470          475          480
80 Ala Asn Val Glu Ala Cys Lys Lys
81          485
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84 <211> LENGTH: 1464
85 <212> TYPE: DNA
86 <213> ORGANISM: Hirudinaria manillensis
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (1)..(1464)
90 <400> SEQUENCE: 2
91 aaa gag att gcc gtg aca att gac gat aag aat gtg att gca tct gcc 48
92 Lys Glu Ile Ala Val Thr Ile Asp Asp Lys Asn Val Ile Ala Ser Ala
93 1 5 10 15
94 agt ggg tct ttc ctt gga gtt gcc ttt gat gcg tct cta ttt tcg ccc 96

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95  Ser Gly Ser Phe Leu Gly Val Ala Phe Asp Ala Ser Leu Phe Ser Pro
96          20          25          30
97  aag ggt ctt tgg agc ttt gtt gat att acc tct cca aaa ttg ttc aaa 144
98  Lys Gly Leu Trp Ser Phe Val Asp Ile Thr Ser Pro Lys Leu Phe Lys
99          35          40          45
100  ttg ctg gaa gga ctt tct cct gga tac ttc agg gtt ggc gga aag ttt 192
101  Leu Leu Glu Gly Leu Ser Pro Gly Tyr Phe Arg Val Gly Gly Thr Phe
102          50          55          60
103  gcc aat tgg ctg ttt ttt gac ttg gac gaa aat aat aag tgg aag gat 240
104  Ala Asn Trp Leu Phe Phe Asp Leu Asp Glu Asn Asn Lys Trp Lys Asp
105  65          70          75          80
106  tat tgg gct ttt aaa gac aaa acc ccc gaa act gcg aca ata aca agg 268
107  Tyr Trp Ala Phe Lys Asp Lys Thr Pro Glu Thr Ala Thr Ile Thr Arg
108          85          90          95
109  aga tgg ctg ttc aga aaa caa aat aat ctg aaa aag gag act ttt gac 336
110  Arg Trp Leu Phe Arg Lys Gln Asn Asn Leu Lys Lys Glu Thr Phe Asp
111          100          105          110
112  aat tta gtg aaa cta aca aag gga agc aag atg aga ttg tta ttc gat 364
113  Asn Leu Val Lys Leu Thr Lys Gly Ser Lys Met Arg Leu Leu Phe Asp
114          115          120          125
115  ttg aat gcc gaa gtg agg act ggt tat gaa att gga aag aag atg aca 432
116  Leu Asn Ala Glu Val Arg Thr Gly Tyr Glu Ile Gly Lys Lys Met Thr
117          130          135          140
118  tcc act tgg gat tca tgg gag gct gaa aag tta ttt aaa tat tgt gtg 480
119  Ser Thr Trp Asp Ser Ser Glu Ala Glu Lys Leu Phe Lys Tyr Cys Val
120  145          150          155          160
121  tca aaa ggt tac gga gac aat atc gat tgg gaa ctt gga aat gaa ccg 528
122  Ser Lys Gly Tyr Gly Asp Asn Ile Asp Trp Glu Leu Gly Asn Glu Pro
123          165          170          175
124  gac cac acc tca gct cac aat tta act gaa aag cag gtt gga gaa gat 576
125  Asp His Thr Ser Ala His Asn Leu Thr Glu Lys Gln Val Gly Glu Asp
126          180          185          190
127  ttt aaa gca ctg cat aaa gtt cta gag aaa tat cca act ctt aac aag 624
128  Phe Lys Ala Leu His Lys Val Leu Glu Lys Tyr Pro Thr Leu Asn Lys
129          195          200          205
130  gga tgg ctg gtt ggt cca gat gta ggg tgg atg ggc gtc agt wac gtc 672
131  Gly Ser Leu Val Gly Pro Asp Val Gly Trp Met Gly Val Ser Tyr Val
132          210          215          220
133  aag gga ttg gca gac gag gcr ggt gac cat gta ack gct ttt aca ctg 720
134  Lys Gly Leu Ala Asp Glu Ala Gly Asp His Val Thr Ala Phe Thr Leu
135  225          230          235          240
136  cac caa tat tat ttc gat gga aac acy tct gat gta tca ata tat ctt 768
137  His Gln Tyr Tyr Phe Asp Gly Asn Thr Ser Asp Val Ser Ile Tyr Leu
138          245          250          255
139  gat gcc aca tac ttt aag aag ctg caa caa cta ttt gat aaa gtg aaa 816
140  Asp Ala Thr Tyr Phe Lys Lys Leu Gln Gln Leu Phe Asp Lys Val Lys
141          260          265          270
142  gat gtt ttg aaa gat tct cca cat aaa gac gaa cca tta tgg ctt gga 864
143  Asp Val Leu Lys Asp Ser Pro His Lys Asp Glu Pro Leu Trp Leu Gly

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144          275          280          285
145 gaa aca agt tct gga tac aac agc ggc aca gaa gat gta tcc gat cga 912
146 Glu Thr Ser Ser Gly Tyr Asn Ser Gly Thr Glu Asp Val Ser Asp Arg
147          290          295          300
148 tat gtt tca gga ttt cta aca tta gac aag ttg ggt ctc agt gca gcc 960
149 Tyr Val Ser Gly Phe Leu Thr Leu Asp Lys Leu Gly Leu Ser Ala Ala
150          305          310          315          320
151 aac aat gta aag gtt gtt ata aga cag aca ata tac aat gga tat tat 1008
152 Asn Asn Val Lys Val Val Ile Arg Gln Thr Ile Tyr Asn Gly Tyr Tyr
153          325          330          335
154 ggt ctc ctt gac aaa aac act tta gag ccg aat ccg gat tac tgg tta 1056
155 Gly Leu Leu Asp Lys Asn Thr Leu Glu Pro Asn Pro Asp Tyr Trp Leu
156          340          345          350
157 atg cat gtt cat aat tct ttg gtc gga aat aca gtt ttt aaa gtt gac 1104
158 Met His Val His Asn Ser Leu Val Gly Asn Thr Val Phe Lys Val Asp
159          355          360          365
160 gtt agt gat cca act aat aaa gca aga gtt tac gcg caa tgt acc aaa 1152
161 Val Ser Asp Pro Thr Asn Lys Ala Arg Val Tyr Ala Gln Cys Thr Lys
162          370          375          380
163 aca aat agc aaa cat act caa agc aga tat tac aag ggc tct ttg aca 1200
164 Thr Asn Ser Lys His Thr Gln Ser Arg Tyr Tyr Lys Gly Ser Leu Thr
165          385          390          395          400
166 atc ttt gca ctt aat gtt gga gat gga gat gta acg tta aag atc ggt 1248
167 Ile Phe Ala Leu Asn Val Gly Asp Gly Asp Val Thr Leu Lys Ile Gly
168          405          410          415
169 caa tac agc ggt aaa aaa att tat tca tac att ctg aca cct gaa gga 1296
170 Gln Tyr Ser Gly Lys Lys Ile Tyr Ser Tyr Ile Leu Thr Pro Glu Gly
171          420          425          430
172 gga caa ctt aca tca cag aaa gtt ctc ttg aat gga aag gaa ttg aac 1344
173 Gly Gln Leu Thr Ser Gln Lys Val Leu Leu Asn Gly Lys Glu Leu Asn
174          435          440          445
175 tta gtg tct gat cag tta cca gaa cta aat gca gat gaa tcc aaa aca 1392
176 Leu Val Ser Asp Gln Leu Pro Glu Leu Asn Ala Asp Glu Ser Lys Thr
177          450          455          460
178 tct ttc acc tta tcc cca aag aca ttt ggt ttt ttt gtt gtt tcc gat 1440
179 Ser Phe Thr Leu Ser Pro Lys Thr Phe Gly Phe Phe Val Val Ser Asp
180          465          470          475          480
181 gct aat gtt gaa gca tgy aar aar 1464
182 Ala Asn Val Glu Ala Cys Lys Lys
183          485
185 <210> SEQ ID NO: 3
186 <211> LENGTH: 488
187 <212> TYPE: PRT
188 <213> ORGANISM: Hirudinaria manillensis
189 <220> FEATURE:
190 <221> NAME/KEY: variation
191 <222> LOCATION: (223)
192 <223> OTHER INFORMATION: May be Asn
193 <400> SEQUENCE: 3

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Please Correct any
Similar Error
in Subsequent Sequences

(See p-5)
"Tyr" is at location 223. Tyr can
only represent itself nothing
else. Use Xaa and explain in
L2207 - L2237 section.

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194 Lys Glu Ile Ala Val Thr Ile Asp Asp Lys Asn Val Ile Ala Ser Ala
195      1              5              10              15
196 Ser Gly Ser Phe Leu Gly Val Ala Phe Asp Ala Ser Leu Phe Ser Pro
197      20              25              30
198 Lys Gly Leu Trp Ser Phe Val Asp Ile Thr Ser Pro Lys Leu Phe Lys
199      35              40              45
200 Leu Leu Glu Gly Leu Ser Pro Gly Tyr Phe Arg Val Gly Gly Thr Phe
201      50              55              60
202 Ala Asn Trp Leu Phe Phe Asp Leu Asp Glu Asn Asn Lys Trp Lys Asp
203      65              70              75              80
204 Tyr Trp Ala Phe Lys Asp Lys Thr Pro Glu Thr Ala Thr Ile Thr Arg
205      85              90              95
206 Arg Trp Leu Phe Arg Lys Gln Asn Asn Leu Lys Lys Glu Thr Phe Asp
207      100             105             110
208 Asn Leu Val Lys Leu Thr Lys Gly Ser Lys Met Arg Leu Leu Phe Asp
209      115             120             125
210 Leu Asn Ala Glu Val Arg Thr Gly Tyr Glu Ile Gly Lys Lys Met Thr
211      130             135             140
212 Ser Thr Trp Asp Ser Ser Glu Ala Glu Lys Leu Phe Lys Tyr Cys Val
213      145             150             155             160
214 Ser Lys Gly Tyr Gly Asp Asn Ile Asp Trp Glu Leu Gly Asn Glu Pro
215      165             170             175
216 Asp His Thr Ser Ala His Asn Leu Thr Glu Lys Gln Val Gly Glu Asp
217      180             185             190
218 Phe Lys Ala Leu His Lys Val Leu Glu Lys Tyr Pro Thr Leu Asn Lys
219      195             200             205
220 Gly Ser Leu Val Gly Pro Asp Val Gly Trp Met Gly Val Ser (Tyr) Val
221      210             215             220
222 Lys Gly Leu Ala Asp Glu Ala Gly Asp His Val Thr Ala Phe Thr Leu
223      225             230             235             240
224 His Gln Tyr Tyr Phe Asp Gly Asn Thr Ser Asp Val Ser Ile Tyr Leu
225      245             250             255
226 Asp Ala Thr Tyr Phe Lys Lys Leu Gln Gln Leu Phe Asp Lys Val Lys
227      260             265             270
228 Asp Val Leu Lys Asp Ser Pro His Lys Asp Glu Pro Leu Trp Leu Gly
229      275             280             285
230 Glu Thr Ser Ser Gly Tyr Asn Ser Gly Thr Glu Asp Val Ser Asp Arg
231      290             295             300
232 Tyr Val Ser Gly Phe Leu Thr Leu Asp Lys Leu Gly Leu Ser Ala Ala
233      305             310             315             320
234 Asn Asn Val Lys Val Val Ile Arg Gln Thr Ile Tyr Asn Gly Tyr Tyr
235      325             330             335
236 Gly Leu Leu Asp Lys Asn Thr Leu Glu Pro Asn Pro Asp Tyr Trp Leu
237      340             345             350
238 Met His Val His Asn Ser Leu Val Gly Asn Thr Val Phe Lys Val Asp
239      355             360             365
240 Val Ser Asp Pro Thr Asn Lys Ala Arg Val Tyr Ala Gln Cys Thr Lys
241      370             375             380
242 Thr Asn Ser Lys His Thr Gln Ser Arg Tyr Tyr Lys Gly Ser Leu Thr

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VERIFICATION SUMMARY

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